

SEQUENCE LISTING

<110> Ebner, Reinhard

Chopra, Arvind

Ruben, Steven M.

<120> Connective Tissue Growth Factor-3

<130> 1488.0630002

<150> US 60/030,720

<151> 1996-11-08

<150> US 08/966,020

<151> 1997-11-07

<160> 13

<170> PatentIn version 3.0

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<213> Homo sapiens

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 Leu Cys Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys
 -5 10 15 20 25
 acc tgc ccc tgg cca cct ccc cga tgc ccg ctg gga gta ccc ctg gtg
 Thr Cys Pro Trp Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val
 15 20 25
 ctg gat ggc tgg ggc tgc tgc cgg gta tgt gca cgg cgg ctg ggg gag
 Leu Asp Gly Cys Gly Cys Arg Val Cys Ala Arg Leu Gly Glu
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 ccc tgc gac caa ctc cac gtc tgc gac gcc agc cag ggc ctg gtc tgc
 Pro Cys Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys
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 cag ccc ggg gca gga ccc ggt ggc cgg ggg gcc ctg tgc ctc ttg gca
 Gln Pro Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala
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 Glu Asp Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly
 80 85 90
 gag acc ttc cag ccc cac tgc agc atc cgc tgc cgc tgc gag gac ggc
 Glu Thr Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly
 95 100 105
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 Gly Phe Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser
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 Trp Asp Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys
 125 130 135
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 Pro Glu Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu
 140 145 150 155
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 Pro Ala Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro
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 175 180 185 190

Gly Val Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr		
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Thr Cys Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe		
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Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Pro		
205	210	215
ccc tcc agg ggt cgc agt cca caa aac agt gcc ttc tagagccgg		768
Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe		
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Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp
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Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys
30 35 40 45

Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro
50 55 60

Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp
65 70 75

Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly Glu Thr
80 85 90

Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly Gly Phe
95 100 105

Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
110 115 120 125

Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys Pro Glu
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Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu Pro Ala
145 150 155

Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro Gly Val
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Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys
175 180 185

Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Arg
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35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
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Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
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Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
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Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
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Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
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Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
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Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
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Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
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Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
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Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
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36

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32

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<400> 6

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ggtctgtntg gatcccagg tatggcagag gtgcaagacc tagtcctctt tcctctaact	180
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cgctgggagt acccctggtg ctggatggct gtggctgctg ccggngttat gtgcacggcg 180
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gcccactccc tgcctacaca cacagcctat atcaaacatg cacacggcg agctttctct 180
ccgacttccc ctggcaaga gatggacaa gcagtccctt aatattgagg ctgcagcagg 240
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Ⓐ

Ⓐ

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